2/52	3/52
Fig.1(i)	Fig.1(ii)
4/52	5/52
Fig.1(iii)	Fig.1(iv)

```
CTG TCT TGG GTG CAT TGG AGC                    49
Leu Ser Trp Val His Trp Ser
 5                      10

CAT GCC AAG TGG TCC CAG GCT GCA                97
His Ala Lys Trp Ser Gln Ala Ala
 20                      25

AAT CAT CAC GAA GTG GTG AAG TTC               145
Asn His His Glu Val Val Lys Phe
                    40

TGC CAT CCA ATC GAG ACC CTG GTG               193
Cys His Pro Ile Glu Thr Leu Val
            55

GAG ATC GAG TAC ATC TTC AAG CCA               241
Glu Ile Glu Tyr Ile Phe Lys Pro
            70                  75

GGG GGC TGC TGC AAT GAC GAG GGC               289
Gly Gly Cys Cys Asn Asp Glu Gly
        85                  90

TCC AAC ATC ACC ATG CAG ATT ATG               337
Ser Asn Ile Thr Met Gln Ile Met
100                     105

CAC ATA GGA GAG ATG AGC TTC CTA               385
His Ile Gly Glu Met Ser Phe Leu
                    120
```

Fig.1(ii)

```
  1        TCGGCCTCC GAAACC ATG AAC TTT CTG
                            Met Asn Phe Leu
                             1

 50        CTT GCC TTG CTG CTC TAC CTC CAC
           Leu Ala Leu Leu Leu Tyr Leu His
                         15

 98        CCC ATG GCA GAA GGA GGA GGG CAG
           Pro Met Ala Glu Gly Gly Gly Gln
                     30                   35

146        ATG GAT GTC TAT CAG CGC AGC TAC
           Met Asp Val Tyr Gln Arg Ser Tyr
                 45                   50

194        GAC ATC TTC CAG GAG TAC CCT GAT
           Asp Ile Phe Gln Glu Tyr Pro Asp
           60                   65

242        TCC TGT GTG CCC CTG ATG CGA TGC
           Ser Cys Val Pro Leu Met Arg Cys
                             80

290        CTC GAG TGT GTG CCC ACT GAG GAG
           Leu Glu Cys Val Pro Thr Glu Glu
                             95

338        CGG ATC AAA CCT CAC CAA GGC CAG
           Arg Ily Lys Pro His Gln Gly Gln
                     110                  115
```

Fig.1(i)

```
386     CAG CAC AAC AAA TGT GAA TGC AGA
        Gln His Asn Lys Cys Glu Cys Arg
            125                 130

434     GAA AAT CCC TGT GGG CCT TGC TCA
        Glu Asn Pro Cys Gly Pro Cys Ser
        140                 145

482     CAA GAT CCG CAG ACG TGT AAA TGT
        Gln Asp Pro Gln Thr Cys Lys Cys
                        160

530     TGC AAG GCG AGG CAG CTT GAG TTA
        Cys Lys Ala Arg Gln Leu Glu Leu
                    175

578     AAG CCG AGG CGG TGAGCCGGGC AGGAG
        Lys Pro Arg Arg
                190

630     GAACCAGATC TCTCACCAGG
```

Fig.1(iii)

```
CCA AAG AAA GAT AGA GCA AGA CAA          433
Pro Lys Lys Asp Arg Ala Arg Gln
            135

GAG CGG AGA AAG CAT TTG TTT GTA          481
Glu Arg Arg Lys His Leu Phe Val
        150                 155

TCC TGC AAA AAC ACA GAC TCG CGT          529
Ser Cys Lys Asn Thr Asp Ser Arg
        165                 170

AAC GAA CGT ACT TGC AGA TGT GAC          577
Asn Glu Arg Thr Cys Arg Cys Asp
180                 185

GAAGG AGCCTCCCTC AGCGTTTCGG              629


                                         649
```

Fig.1(iv)

7/52 Fig.2(i)	8/52 Fig.2(ii)
9/52 Fig 2(iii)	10/52 Fig 2(iv)
11/52 Fig 2(v)	12/52 Fig 2(vi)

```
 1        CC ATG AGC CCT CTG CTC CGC CGC
             Met Ser Pro Leu Leu Arg Arg
              1                    5

48        CTG GCC CCC GCC CAG GCC CCT GTC
          Leu Ala Pro Ala Gln Ala Pro Val
                             20

96        CAG AGG AAA GTG GTG TCA TGG ATA
          Gln Arg Lys Val Val Ser Trp Ile
                         35

144       CAG CCC CGG GAG GTG GTG GTG CCC
          Gln Pro Arg Glu Val Val Val Pro
                      50                  55

192       GTG GCC AAA CAG CTG GTG CCC AGC
          Val Ala Lys Gln Leu Val Pro Ser
                  65                  70

240       GGC TGC TGC CCT GAC GAT GGC CTG
          Gly Cys Cys Pro Asp Asp Gly Leu
           80                  85

288       CAA GTC CGG ATG CAG ATC CTC ATG
          Gln Val Arg Met Gln Ile Leu Met
                          100

336       GGG GAG ATG TCC CTG GAA GAA CAC
          Gly Glu Met Ser Leu Glu Glu His
                      115
```

Fig.2(i)

```
CTG CTG CTC GCC GCA CTC CTG CAG        47
Leu Leu Leu Ala Ala Leu Leu Gln
         10                  15

TCC CAG CCT GAT GCC CCT GGC CAC        95
Ser Gln Pro Asp Ala Pro Gly His
     25                  30

GAT GTG TAT ACT CGC GCT ACC TGC       143
Asp Val Tyr Thr Arg Ala Thr Cys
40                  45

TTG ACT GTG GAG CTC ATG GGC ACC       191
Leu Thr Val Glu Leu Met Gly Thr
             60

TGC GTG ACT GTG CAG CGC TGT GGT       239
Cys Val Thr Val Gln Arg Cys Gly
         75

GAG TGT GTG CCC ACT GGG CAG CAC       287
Glu Cys Val Pro Thr Gly Gln His
         90                  95

ATC CGG TAC CCG AGC AGT CAG CTG       335
Ile Arg Tyr Pro Ser Ser Gln Leu
    105                 110

AGC CAG TGT GAA TGC AGA CCT AAA       383
Ser Gln Cys Glu Cys Arg Pro Lys
120                 125
```

Fig. 2(ii)

```
384    AAA AAG GAC AGT GCT GTG AAG CCA
       Lys Lys Asp Ser Ala Val Lys Pro
               130                     135

432    CGT CCC CAG CCC CGT TCT GTT CCG
       Arg Pro Gln Pro Arg Ser Val Pro
           145                     150

480    CCC TCC CCA GCT GAC ATC ACC CAT
       Pro Ser Pro Ala Asp Ile Thr His
       160                     165

528    GCC CAC GCT GCA CCC AGC ACC ACC
       Ala His Ala Ala Pro Ser Thr Thr
                       180

576    GCT GCC GCT GCC GAC GCC GCA GCT
       Ala Ala Ala Ala Asp Ala Ala Ala
                       195
```

Fig. 2(iii)

```
GAC  AGG  GCT  GCC  ACT  CCC  CAC  CAC       431
Asp  Arg  Ala  Ala  Thr  Pro  His  His
                    140

GGC  TGG  GAC  TCT  GCC  CCC  GGA  GCA       479
Gly  Trp  Asp  Ser  Ala  Pro  Gly  Ala
                    155

CCC  ACT  CCA  GCC  CCA  GGC  CCC  TCT       527
Pro  Thr  Pro  Ala  Pro  Gly  Pro  Ser
               170                      175

AGC  GCC  CTG  ACC  CCC  GGA  CCT  GCC       575
Ser  Ala  Leu  Thr  Pro  Gly  Pro  Ala
          185                      190

TCC  TCC  GTT  GCC  AAG  GGC  GGG  GCT  T    624
Ser  Ser  Val  Ala  Lys  Gly  Gly  Ala
200                      205
```

Fig.2(iv)

625   AGAGCTCAAC CCAGACACCT GCAGGTGCCG

685   GACTCAGCAG GGTGACTTGC CTCAGAGGCT

745   GGTAAAAAAC AGCCAAGCCC CCAAGACCTC

805   GCCTCTCAGA GGGCTCTTCT GCCATCCCTT

865   GAGTTGGAAG AGGAGACTGG GAGGCAGCAA

825   GGAGTACTGT CTCAGTTTCT AACCACTCTG

985   CTCCCCTCAC TAAGAAGACC CAAACCTCTG

1045   CTGTGACCCC CAACCCTGAT AAAAGAGATG

Fig.2(v)

GAAGCTGCGA AGGTGACACA TGGCTTTTCA 684

ATATCCCAGT GGGGGAACAA AGGGGAGCCT 744

AGCCCAGGCA GAAGCTGCTC TAGGACCTGG 804

GTCTCCCTGA GGCCATCATC AAACAGGACA 864

GAGGGGTCAC ATACCAGCTC AGGGGAGAAT 924

TGCAAGTAAG CATCTTACAA CTGGCTCTTC 984

CATAATGGGA TTTGGGCTTT GGTACAAGAA 1044

GAAGGAAAAA AAAAAAAAAA 1094

Fig.2(vi)

14/52	15/52
Fig. 3(i)	*Fig. 3(ii)*

>VEGF_HUMAN VEGF_HUMAN VASCULAR ENDOTHELIAL
(VASCULAR 215 AA.
LENGTH = 215

SCORE = 181 (92.4 BITS), EXPECT = 6.4e-20,
IDENTITIES = 33/75 (44%), POSITIVES = 48/75

QUERY: 31 HQRKVVSWIDVYTRATCQPREVVVPLTVEL
               +++ VV   +DVY R+ C+P E +V + E
SBJCT: 36 NHHEVVKFMDVYQRSYCHPIETLVDIFQEY

QUERY: 91 PTGQHQVRMQILMIR 105
               PT +   + MQI+ I+
SBJCT: 96 PTEESNITMQIMRIK 110

SCORE = 76 (38.8 BITS), EXPECT = 0.0011,
IDENTITIES = 12/19 (63%), POSITIVES = 16/19

QUERY: 110 QLGEMSLEEHSQCECRPKK 128
               ++GEMS +H+ CECRPKK
SBJCT: 116 HIGEMSFLQHNKCECRPKK 134

SCORE = 72 (36.8 BITS), EXPECT = 0.0046,
IDENTITIES = 14/21 (66%), POSITIVES = 15/21

QUERY: 202 RCQGRGLELNPDTCRCRKLRR 222
               RC +R LELN TCRC K RR
SBJCT: 195 RCKARQLELNERTCRCDKPRR 215

SCORE = 46 (23.5 BITS), EXPECT = 47.,
IDENTITIES = 6/10 (60%), POSITIVES = 9/10

QUERY: 187 DPRTCRCRCR 196
               DP+TC+C C+
SBJCT: 181 DPQTCKCSCK 190

Fig.3(i)

GROWTH FACTOR PRECURSOR (VEGF)

P = 6.4e-20
(64%)

MGTVAKQLVPSCVTVQRCGGCCPDDGLECV 90
   +   PSCV + RCGGCC D+GLECV
PDEIEYIFKPSCVPLMRCGGCCNDEGLECV 95

POISSON P(2) = 9.1e-12
(84%)

POISSON P(3) = 3.6e-18
(71%)

POISSON P(4) = 7.3e-10
(90%)

Fig. 3(i)

17/52 Fig.4(i)	18/52 Fig.4(ii)
19/52 Fig.4(iii)	20/52 Fig.4(iv)

Gap Weight:3.00   Average Match:1.000
Length Weight:0.100   Average Mismatch:-0.900
        Quality:100.9   Length:739
          Ratio:0.175   Gaps:30
    Percent   Percent
Similarity:69.703   Identity:69.703

```
 28    ATGAGCCCTCTGCTCCGCCGCCTGC
       ||||  |   ||||||        |  ||
 17    ATGAACTTTCTGCT.....GTCT..

 68    TGCAGCTGGCCCCCGCCCAGGCCCC
       |||  |||    ||  |   |||  |||
 57    TGCTGCTCTACCTCCACCATGCCAA

118    CACCAGAGGA................
          |||||
106    AGAAGGAGGAGGGCAGAATCATCAC

140    GTGTATACTCGC.GCTACCTGCCAG
       ||  |||    |||  ||||  ||||||
152    GTCTATCAGCGCAGCTA.CTGCCAT

194    T....GA.....CTGTGGAGCTCAT
       |     ||         |||   |||  ||
201    TCCAGGAGTACCCTGATGAGATCGA

235    CCCAGCTGCGTGACTGTGCAGCGCT
       ||    |||  |||  |    ||    |||  |
239    CCATCCTGTGTGCCCCTGATGCGAT

285    CCTGGAGTGTGTGCCCACTGGGCAG
       |||||||||||||||||||||||  |  ||
289    CCTGGAGTGTGTGCCCACTGAGGAG
```

Fig.4(i)

```
TGCTCGCCGCACT..........CC          67
 |  |   ||| |            |
...TGGGTGCATTGGAGCCTTGCCT          56


TGTCTCCCAGCCTGATGCCCCTGGC         117
   ||||||  |||     |||  ||||
GTGGTCCCAGGCTGCA.CCCATGGC         105


.AAGTGGTG....TCATGGATAGAT         147
 ||||||||     |||||    |||
GAAGTGGTGAAGTTCATG....GAT         151


CCCCGGGAG...GTGGTGGTGCCCT         193
||     |||   ||||||     ||
CCAATCGAGACCCTGGTGGACATCT         200


GGGCACCGTGGCCAAACAGCTGGTG         234
|  || | |    |||          |
GTACATCTT...CAA.........G         238


GTGGTGGCTGCTGCCCTGACGATGG         284
| ||  ||||||||||  |||||||  ||
GCGGGGGCTGCTGCAATGACGAGGG         288


CACCAAGTCCGGATGCAGAT.....         329
  | |   ||    |||||||||
TCCAACATCACCATGCAGATTATGC         338
```

Fig.4(ii)

```
330    . . . . . . . . .CCTCATGATCCGGTACC
                        | | | | |                    |
339    GGATCAAACCTCA. . . . . . . . . . .C

369    GTCCCTGGAAGAACACAGCCAGTGT
       |   |   |     |   |   | | | |   |   |   | | |
376    GAGCTTCCTACAGCACAACAAATGT

419    GTGCTGTGAAGCCAGACAGGGCTGC
       |               | | |   | | | | |   |
423    G. . . . . . . .AGCAAGACAAG. . . . .

469    CGTTCTGTTCCGGGCTGGGACTCTG
          |   | |     | |     | | |     | |
443    . . .TGTGGGCCTTGCTCAGA. . . . .

519    CATCACCCATCCCACTCCAGCCCCA

468    . . . . . . . . . . . . . . . . . . . . . . . . .

569    GC. . . . . . . . . . .ACCACCAGCGCCC
       | |                        | |   |
469    GCATTGTTTGTACAA. . . . . . . . .

609    TGCCGACGCCGCAGCTTCCTCCGTT
       | |   |   |       |   | | |     | |       | | | |
509    TG.CAAAAACACAGACTC. .GCGTT

657    AACCCAGACACCTGCAGGTGCCGGA
       | | |       |
554    AACGAACGTACTTGCAGATGTGACA
```

Fig.4(iii)

```
CGAGCAGTCAGC . . . TGGGGGAGAT          368
 |  | |    |   | | |||        |  | | |||||
CAAG . . GCCAGCACATAGGAGAGAT          375


GAATGCAGACCTAAAAAAAAGGACA          418
||||||||||||       |||  ||   ||  |
GAATGCAGACC . . . AAAGAAAGATA          422


CACTCCCCACCACCGTCCCCAGCCC          468
                |      ||||
 . . . . . . . . . . . . AAAATCCC . . . . . .          442


CCCCCGGAGCACCCTCCCCAGCTGA          518
      |||||| |
 . . . GCGGAGAA . . . . . . . . . . . . . .          467


GGCCCCTCTGCCCACGCTGCACCCA          568
                                 |
 . . . . . . . . . . . . . . . . . . . . . . . . A          468


TGACCCCCGGACCTGCCGCTGCCGC          608
 || || |  ||| ||       ||      |
 . GATCCGCAGACGTGTAAATGTTCC          508


GCCAAGGGCGGGGC . . TTAGAGCTC          656
||      ||||  |||    |  |||  |
GC . . AAGGCGAGGCAGCTTGAGTTA          553


AGCTGCGAAGGTGA          695


AGCCGAGGCGGTGA          592
```

Fig. 4 (iv)

SUBSTITUTE SHEET (RULE 26)

22/52	23/52	24/52
Fig.5(i)	Fig.5(ii)	Fig.5(iii)
25/52	26/52	27/52
Fig.5(iv)	Fig.5(v)	Fig.5(vi)

165SOMSQ.MSF.msf MSF:687
Type: D Tuesday, June 20, 1995
Check:3140

```
                         1
      VEGF165    ATGAACTTTCTGCTGTCTTGGGTG
       SOM175    ATGAGCCCTCTGCTCCGCCGCCTG
    SOM175-e6    ATGAGCCCTCTGCTCCGCCGCCTG
  SOM175-e6&7    ATGAGCCCTCTGCTCCGCCGCCTG
    SOM175-e4    ATGAGCCCTCTGCTCCGCCGCCTG


                        81
      VEGF165    CACCCATGGCAGAAGGAGGAGGGC
       SOM175    TGCCCCTGGCCACCAGAGGAAAGT
    SOM175-e6    TGCCCCTGGCCACCAGAGGAAAGT
  SOM175-e6&7    TGCCCCTGGCCACCAGAGGAAAGT
    SOM175-e4    TGCCCCTGGCCACCAGAGGAAAGT


                       161
      VEGF165    CCAATCGAGACCCTGGTGGACATC
       SOM175    GTGGTGGTGCCCTTGACTG.TGGA
    SOM175-e6    GTGGTGGTGCCCTTGACTG.TGGA
  SOM175-e6&7    GTGGTGGTGCCCTTGACTG.TGGA
    SOM175-e4    GTGGTGGTGCCCTTGACTG.TGGA


                       241
      VEGF165    GATGCGATGCGGGGGCTGCTGCAA
       SOM175    GCAGCGCTGTGGTGGCTGCTGCCC
    SOM175-e6    GCAGCGCTGTGGTGGCTGCTGCCC
  SOM175-e6&7    GCAGCGCTGTGGTGGCTGCTGCCC
    SOM175-e4    GCAGCGCTGTGGTGGCTGCTGCCC
```

Fig.5(i)

```
CATTGGAGCCTTGCCTTGCTGCTCTACC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC


AGAATCATCACGAAGTGGTGAAGTTCAT
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC


TTCCAGGAGTACCCTGATGAGATCGAGT
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC


TGACGAGGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
```

Fig. 5(ii)

```
                                        80
TCCACCATGCCAAGTGGTCCCAGGCTG.
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA

                                        160
GGATGTCTATCAGCGCAGCTACTGCCAT
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG

                                        240
ACATCTTCAAGCCATCCTGTGTGCCCCT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT

                                        320
GAGGAGTCCAACATCACCATGCAGATTA
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGA...
```

Fig.5(iii)

```
                   321
       VEGF165     TGCGGATCAAACCTCACCAAGGCC
        SOM175     TCATGATCCGG...TACCCGAGCA
     SOM175-e6     TCATGATCCGG...TACCCGAGCA
   SOM175-e6&7     TCATGATCCGG...TACCCGAGCA
     SOM175-e4     ........................


                   401
       VEGF165     AAGAAAGATAG........AGCAA
        SOM175     AAAAAGGACAGTGCTGTGAAGCCA
     SOM175-e6     AAAAAGGACAGTGCTGTGAAGCCA
   SOM175-e6&7     AAAAAGGACAGTGCTGTGAAGCCA
     SOM175-e4     AAAAAGGACAGTGCTGTGAAGCCA


                   481
       VEGF165     ...........AAGCA........
        SOM175     CTCTGCCCCCGGAGCACCCTCCCC
     SOM175-e6     ........................
   SOM175-e6&7     ........................
     SOM175-e4     CTCTGCCCCCGGAGCACCCTCCCC


                   561
       VEGF165     A................GATCCGCA
        SOM175     GCACCACCAGCGCCCTGACCCCCG
     SOM175-E6     GCACCACCAGCGCCCTGACCCCCG
   SOM175-e6&7     ........................
     SOM175-e4     GCACCACCAGCGCCCTGACCCCCG


                   641
       VEGF165     TTGAGTTAAACGAACGTACTTGCA
        SOM175     TAGAGCTCAACCCAGACACCTGCA
     SOM175-e6     TAGAGCTCAACCCAGACACCTGCA
   SOM175-e6&7     ........................
     SOM175-e4     TAGAGCTCAACCCAGACACCTGCA
```

Fig.5(iv)

AGCACATAGGAGAGATGAGCTTCCTACA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
. . . .

GACAAGAA. . . .AATCCCTGTGG. . . . .
GACAGGGCTGCCACTCCCCACCACCGTC
GATAG. . . . .
GATAG. . . . .
GACAGGGCTGCCACTCCCCACCACCGTC

. . . .
AGCTGACATCACCCATCCCACTCCAGCC
. CC
. . . .
AGCTGACATCACCCATCCCACTCCAGCC

GACGTGTAAATGTTCCTGCAAAAAC.AC
GACCTGCCGCTGCCGCTGCCGACGCCGC
GACCTGCCGCTGCCGCTGCCGACGCCGC
. . . .
GACCTGCCGCTGCCGCTGCCGACGCCGC

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GATGTGACAAGCCGAGGCGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
.GTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA

Fig.5(v)

```
                                              400
GCACAACAAATGTGAATGCAGACC...A
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
.......................CCTAAA


                                              480
..........GCCTTGCTCAGAGCGGAGA
CCCAGCCCCGTTCTGTTCCGGGCTGGGA
.............................
.............................
CCCAGCCCCGTTCTGTTCCGGGCTGGGA


                                              560
..........TTTGTT.....TGTAC..A
CCAGGCCCCTCTGCCCACGCTGCACCCA
CCAGGCCCCTCTGCCCACGCTGCACCCA
............................
CCAGGCCCCTCTGCCCACGCTGCACCCA


                                              640
AGACTCG..CGTTGCAAGGCGAGGCAGC
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
............................
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
```

Fig.5(vi)

Fig 6(i)

29/52

Fig 6(ii)

30/52

Fig 6(iii)

31/52

VEGF₁₆₅   M N F L L S W V H W S L A L L Y L H H A K W S Q A A P
SOM175 Short   M S P L L R R L L . . L A A L L Q L A P A Q . . A P

VEGF₁₆₅   I F Q E Y P D E I E Y I F K P S C V P L M R C G G C C N
SOM175 Short   L T V E L M G T V A K Q L V P S C V T V Q R C G G C C P

VEGF₁₆₅   F L Q H N K C E C R P K K
SOM175 Short   L E E H S Q C E C R P K K

VEGF₁₆₅   C K C S C K N T D S R C K A R Q L E L N E R T C R C D K
SOM175 Short   . . . . D S A V K P D R A A T P H H

OR....

VEGF₁₆₅   M N F L L S W V H W S L A L L Y L H H A K W S Q A A P
SOM175 Long   M S P L L R R L L . . L A A L L Q L A P A Q . . A P

VEGF₁₆₅   I F Q E Y P D E I E Y I F K P S C V P L M R C G G C C N
SOM175 Long   L T V E L M G T V A K Q L V P S C V T V Q R C G G C C P

VEGF₁₆₅   F L Q H N K C E C R P K K
SOM175 Long   L E E H S Q C E C R P K K

VEGF₁₆₅   G P C S E R R K H L F V Q D P Q T C K C S C K N T D S .
SOM175 Long   P R C T Q H Q R . . P D P R T C R C R R S F L

Fig.6(i)

M A E G G G Q N H E . V V K F M D V Y Q R S Y C H P I E T L V D   60
V S Q P D A P G H Q R K V V S W I D V Y T R A T C P R E V V P   55

D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
D D G L E C V P T G Q H Q V R M Q I L M I R . Y P S S Q L G E M S 115

. R Q E N P C G P C S E R R K H L F . V Q D P Q T   170
. R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P S A 175

P R R 191
G G A 207

M A E G G G Q N H E . V V K F M D V Y Q R S Y C H P I E T L V D   60
V S Q P D A P G H Q R K V V S W I D V Y T R A T C P R E V V P   55

D E G L E C V P T E E S N I T M Q I M R I K P H Q G Q H I G E M S 121
D D G L E C V P T G Q H Q V R M Q I L M I R . Y P S S Q L G E M S 115

R Q E N P . . . R S V P G W D S A P G A P S P A D I T H P T P A P G P L C 170
R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P L C 177

R C K A R Q L E L N E R T C R C D K P R R 191
R C Q G R G L E L N P D T C R C R K L R R 222

Fig. 6(ii)

Areas of 100% homology are boxed and conserved residues thought to be involved in homodimerisation are underlined. The VEGF sequence depicted includes the 26 amino acid leader sequence (removal of which gives rise to mature VEGF$_{165}$) giving a total length of 191 amino acids.

Homology of SOM175 to VEGF$_{165}$ is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF).

ie.   Cysteine-47

Proline-70, Cysteine-72, Valine-74

Arginine-77, Cystein-78, Glycine-80, Cysteines-81 & 82

Cysteine-89, Proline-91

Cysteines 122 & 124

Fig.6(iii)

SPLICE VARIANTS OF SOM175

SOM175

SOM175 MINUS EXON 4

SOM175 MINUS EXON 6

SOM175 MINUS EXON 6 & 7
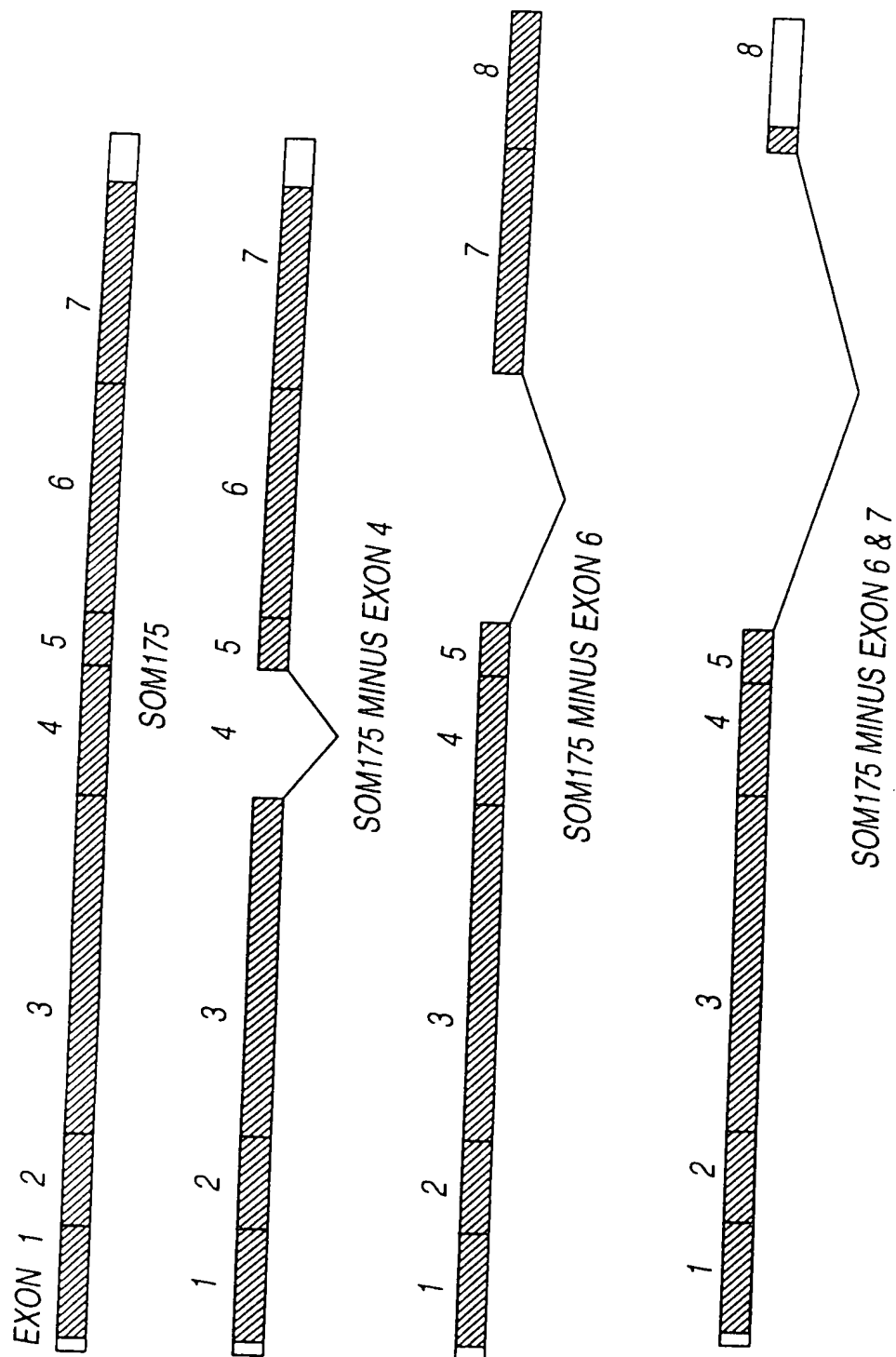
Fig.7

GENOMIC STRUCTURE OF HUMAN SOM175
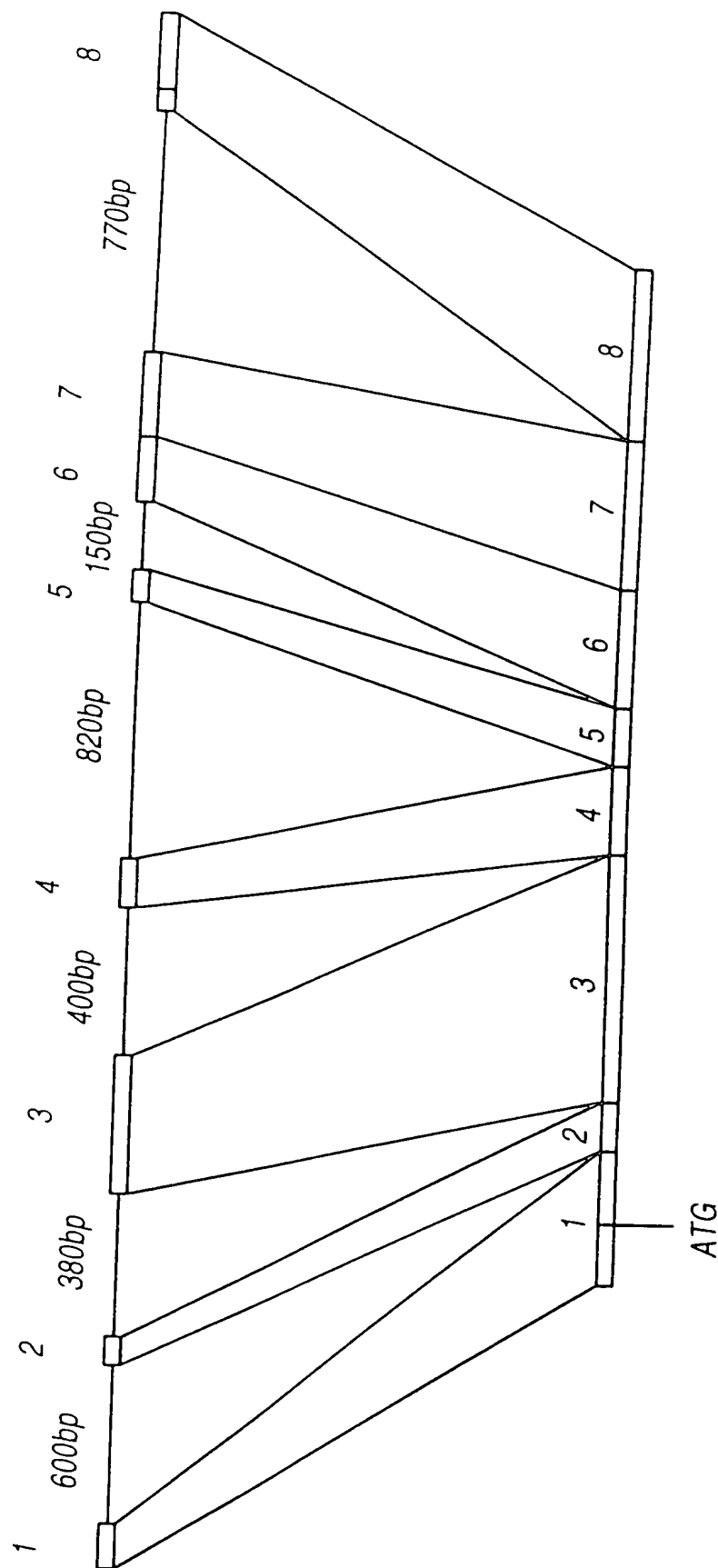
Fig.8A

5'UTR.... **ATGAGG**

tctcccacag GCCCCT   *Exon 1   (60bp)   GGCCAG gtacgtgagg

tctgctccca TGGTGT   Exon 2   (43bp)   GGAAAG aatacttaca

ctgaatacag ATCCTC   Exon 3   (187bp)   ATGCAG gtccgagatg

acttttcaag ACCTAA   Exon 4   (73bp)   ATGCAG gtgtcaggca

ctcctccgta GGCTGC   Exon 5   (34bp)   AGACAG gtgagtcttt

cccactccag CCCCAG   Exon 6   (101bp)   CTCCAG ccccaggccc

ccctgctccag CCCCAG   Exon 7   (109bp)   ACCCAG acacctgtag

ccctgctcag GTGCCG   *Exon 8   (22bp)   **AGGTGA** ...3'UTR

Fig.8B

36/52	37/52
Fig. 9(i)	Fig. 9(ii)
38/52	39/52
Fig. 9(iii)	Fig. 9(iv)

```
-163    gcacgagctcaggccgtcgctgcggcgctg
-103    gggggccgcggaggagccgcccctgcgcc
 -43    ggcggctctggctgaccccccccacaccg


  16    CGTCGCTGCTGCTTGTTGCACTGCTGCAG
         R   R   L   L   L   V   A   L   L   Q


  76    TTTGATGGCCCCAGTCACCAGAAGAAAGTG
         F   D   G   P   S   H   Q   K   K   V


 136    ACATGCCAGCCCAGGGAGGTGGTGGTGCCT
         T   C   Q   P   R   E   V   V   V   P


 196    AAACAACTAGTGCCCAGCTGTGTGACTGTG
         K   Q   L   V   P   S   C   V   T   V


 256    GGCCTGGAATGTGTGCCCACTGGGCAACAC
         G   L   E   C   V   P   T   G   Q   H


 316    TACCCGAGCAGTCAGCTGGGGGAGATGTCC
         Y   P   S   S   Q   L   G   E   M   S


 376    CCTAAAAAAAGGAGAGTGCTGTGAGGCCA
         P   K   K   K   E   S   A   V   R   P


 436    CAGCCCCGCTCTGTTCCGGGCTGGGACTCT
         Q   P   R   S   V   P   G   W   D   S
```

Fig.9(i)

```
cgttgcgctgcctgcgcccagggctcggga
ccgccccgggtccccgggtccgcgccatgg
ccgggctagggcccgATGAGCCCCCTGCTG
                    M   S   P   L   L      -17

CTGGCTCGCACCCAGGCCCCTGTGTCCCAG
 L   A   R   T   Q   A   P   V   S   Q      4

GTGCCATGGATAGACGTTTATGCACGTGCC
 V   P   W   I   D   V   Y   A   R   A      24

CTGAGCATGGAACTCATGGGCAATGTGGTC
 L   S   M   E   L   M   G   N   V   V      44

CAGCGCTGTGGTGGCTGCTGCCCTGACGAT
 Q   R   C   G   G   C   C   P   D   D      64

CAAGTCCGAATGCAGATCCTCATGATCCAG
 Q   V   R   M   Q   I   L   M   I   Q      84

CTGGGAGAACACAGCCAATGTGAATGCAGA
 L   G   E   H   S   Q   C   E   C   R      104

GACAGGGTTGCCATACCCCACCACCGTCCC
 D   R   V   A   I   P   H   H   R   P      124

ACCCCGGGAGCACCCTCCCCAGCTGACATC
 T   P   G   A   P   S   P   A   D   I      144
```

Fig.9(ii)

```
496   ATCCATCCCACTCCAGCCCCAGGATCCTCT
       I   H   P   T   P   A   P   G   S   S
                               S   P   R   I   L

556   CTGACCCCCGGACCTGCCGTTGCCGCTGTA
       L   T   P   G   P   A   V   A   A   V
       P   D   P   R   T   C   R   C   R   C

616   GGGGCTTAGAGCTCAACCCAGACACCTGTA
       G   A   *
       R   G   L   E   L   N   P   D   T   C

676   ctttccagactccacgggcccggctgcttt
736   agcacaggcgtaacctcctcagtctgggag
796   gagctctcgccatcttttatctcccaga
856   atgtctcacctcaggggccagggtactctc
916   ttctggctggctgtctccctcactatgaa
976   gggttctgttatgataactgtgacacacac
1036  gacactaaaaaaaaaaaaaaaaaaaaaaa
```

Fig.9(iii)

```
GCCCGCCTTGCACCCAGCGCCGCCAACGCC
   A   R   L   A   P   S   A   A   N   A        164
 C   P   P   C   T   Q   R   R   Q   R          130

GACGCCGCCGCTTCCTCCATTGCCAAGGGC
   D   A   A   A   S   S   I   A   K   G        184
 R   R   R   R   F   L   H   C   Q   G          150

GGTGCCGGAAGCCGCGAAGTGAcaagctg

 R   C   R   K   P   R   K   *                  186
                                                167

tatggccctgcttcacagggagaagagtgg
gtcactgccccaggacctggaccttttaga
gctgccatctaacaattgtcaaggaacctc
tcacttaaccaccctggtcaagtgagcatc
aaccccaaacttctaccataacgggattt
acacactcacactctgataaaagagatgga
aaaaaaaaaaa
```

Fig.9(iv)

41/52	42/52
Fig 10(i)	Fig 10(ii)
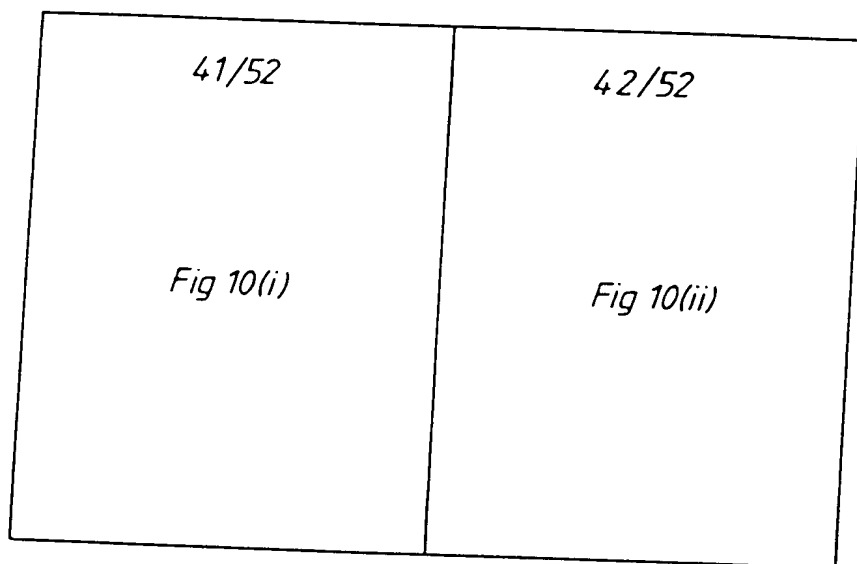
A

hVRF167   -21 MSPLLRRLLLAALLQLAPAQAP
                 ||||||||||||||||||| |||
mVRF167   -21 MSPLLRRLLLVALLQLARTQAP

hVRF167   30 EVVVPLTVELMGTVAKQLVPSC
                 ||||||| :|||| | ||||||||
mVRF167   30 EVVVPLSMELMGNVVKQLVPSC

hVRF167   80 ILMIRYPSSQLGEMSLEEHSQC
                 |||| ||||||||||||:|||||
mVRF167   80 ILMIQYPSSQLGEMSLGEHSQC

hVRF167   130 RPDPRTCRCRCRRRSFLRCQGR
                 ||||||||||||||| ||:||||
mVRF167   130 RPDPRTCRCRCRRRRFLHCQGR

B

hVRF186   116 RAATPHHRPQPRSVPGWDSAPG
                 | ||||||||||||||||| ||
mVRF186   116 RVAIPHHRPQPRSVPGWDSTPG

hVRF186   166 TPGPAAAAADAAASSVAKGGA*
                 ||||| || ||||||:|||||
mVRF186   166 TPGPAVAAVDAAASSIAKGGA*

Fig.10(i)

```
VSQPDAPGHQRKVVSWIDVYTRATCQPR    29
||| |:|:||:||| ||||| |||||||
VSQFDGPSHQKKVVPWIDVYARATCQPR    29

VTVQRCGGCCPDDGLECVPTGQHQVRMQ    79
|||||||||||||||||||||||||||||
VTVQRCGGCCPDDGLECVPTGQHQVRMQ    79

ECRPKKKDSAVKPDSPRPLCPRCTQHHQ   129
|||||||:|||:||||| ||| |||::|
ECRPKKKESAVRPDSPRILCPPCTQRRQ   129

GLELNPDTCRCRKLRR*  167
|||||||||||||||:
GLELNPDTCRCRKPRK*  167




APSPADITHPTPAPGPSAHAAPSTTSAL  165
|||||||| ||||||| ||: |||   ||
APSPADIIHPTPAPGSSARLAPSAANAL  165

186

186
```

Fig. 10(ii)

44/52

Fig 11(i)

45/52

Fig 11(ii)

```
mVRF167      -21  MSPLLRRL..LLVALLQL..
                  |  ||  ::      |: || |
mVEGF188     -26  MNFLLSWVHWTLALLLYLHH


mVRF167       25  TCQPREVVVPLSMELMGNVV
                  | | |  :|  :    |   : ::
mVEGF188      24  YCRPIETLVDIFQEYPDEIE


mVRF167       75  QVRMQILMIQYPSSQ.LGEM
                  :  |||:  |        ||  :|||
mVEGF188      74  NITMQIMRIKPHQSQHIGEM


mVRF167      119  ..............ILCPPC
                              :  |  ||
mVEGF188     124  QKRKRKKSRFKSWSVHCEPC


mVRF167      152  GLELNPDTCRCRKPRK
                  ||||    ||||  |||:
mVEGF188     173  QLELNERTCRCDKPRR
```

Fig.11(i)

```
AR.TQAPVSQFDGPSHQKKVVPWIDVYARA          24
 |:  ||:    :|   :  :  |:  ::||| |
AKWSQAAPTT.EGEQKSHEVIKFMDVYQRS          23

KQLVPSCVTVQRCGGCCPDDGLECVPTGQH          74
 :  ||||  :  ||:|||  |::|||||| ::
YIFKPSCVPLMRCAGCCNDEALECVPTSES          73

SLGEHSQCECRPKKKESAVRPDSPR.....          118
|:  :||  |||||||          | |
SFLQHSRCECRPKKDRTKPEKKSVRGKGKG          123

TQRRQR...PDPRTCRCRCRRRRFLHCQGR          151
 :||  :       ||  ||:| |:     :| :|
SERRKHLFVQDPQTCKCSCKNTDS.RCKAR          172

                                        167

                                        188
```

Fig. 11 (ii)
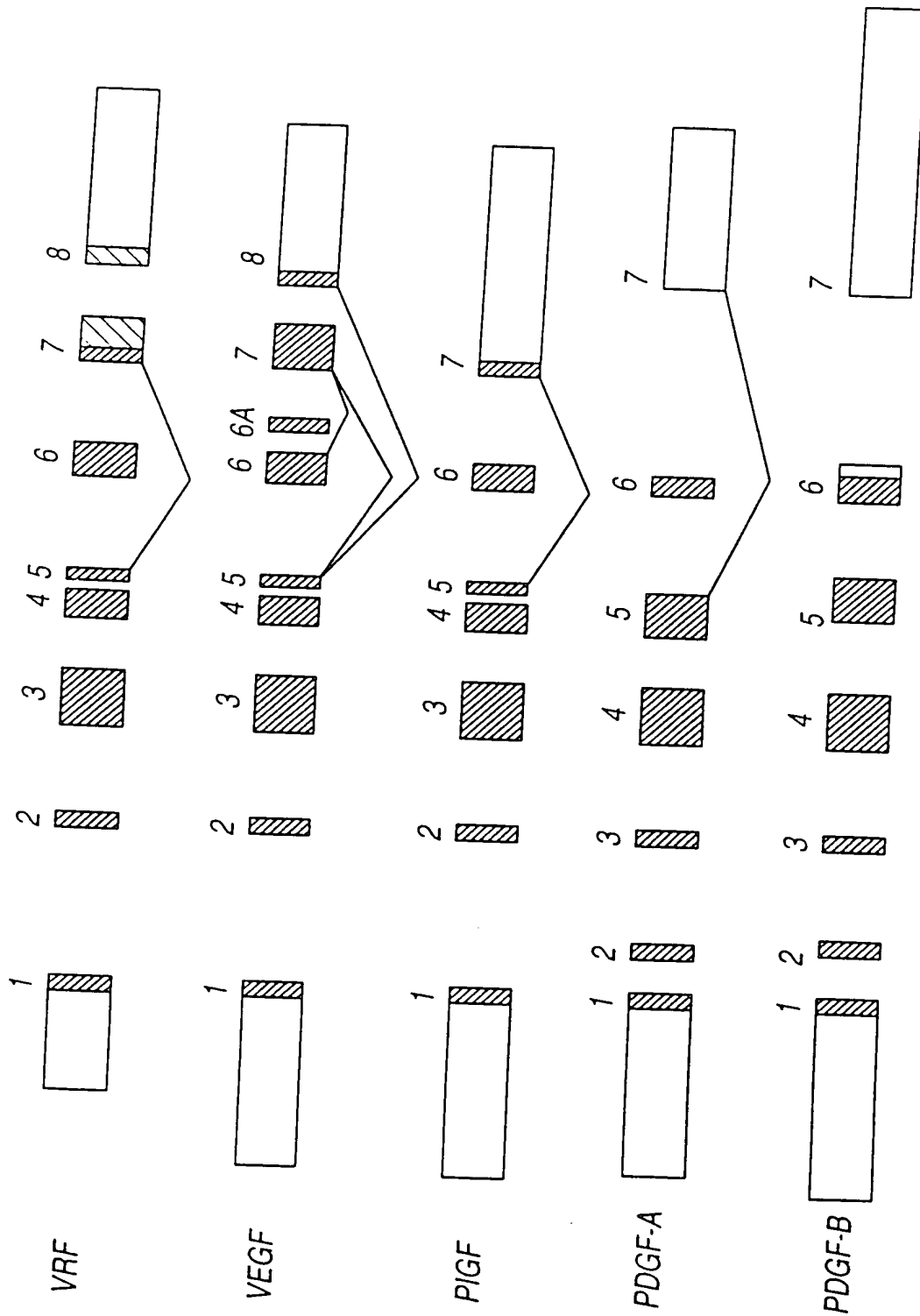
Fig.12
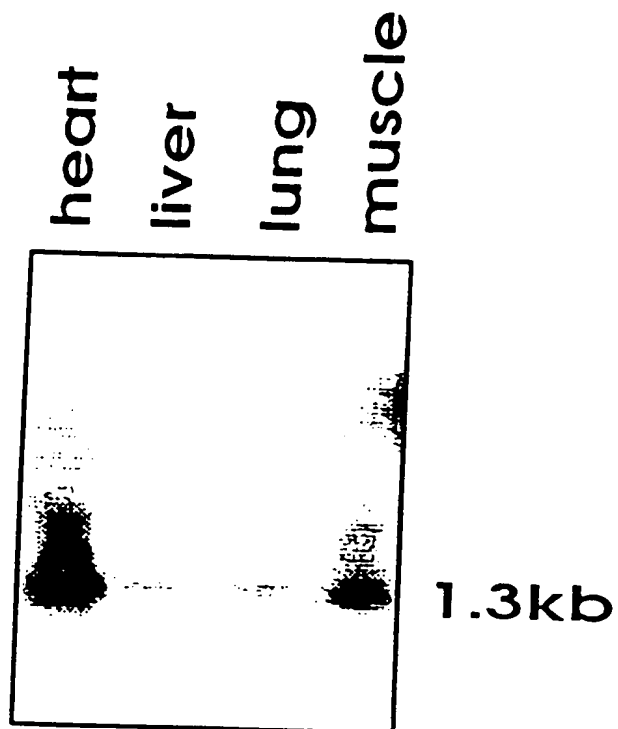
Fig.13
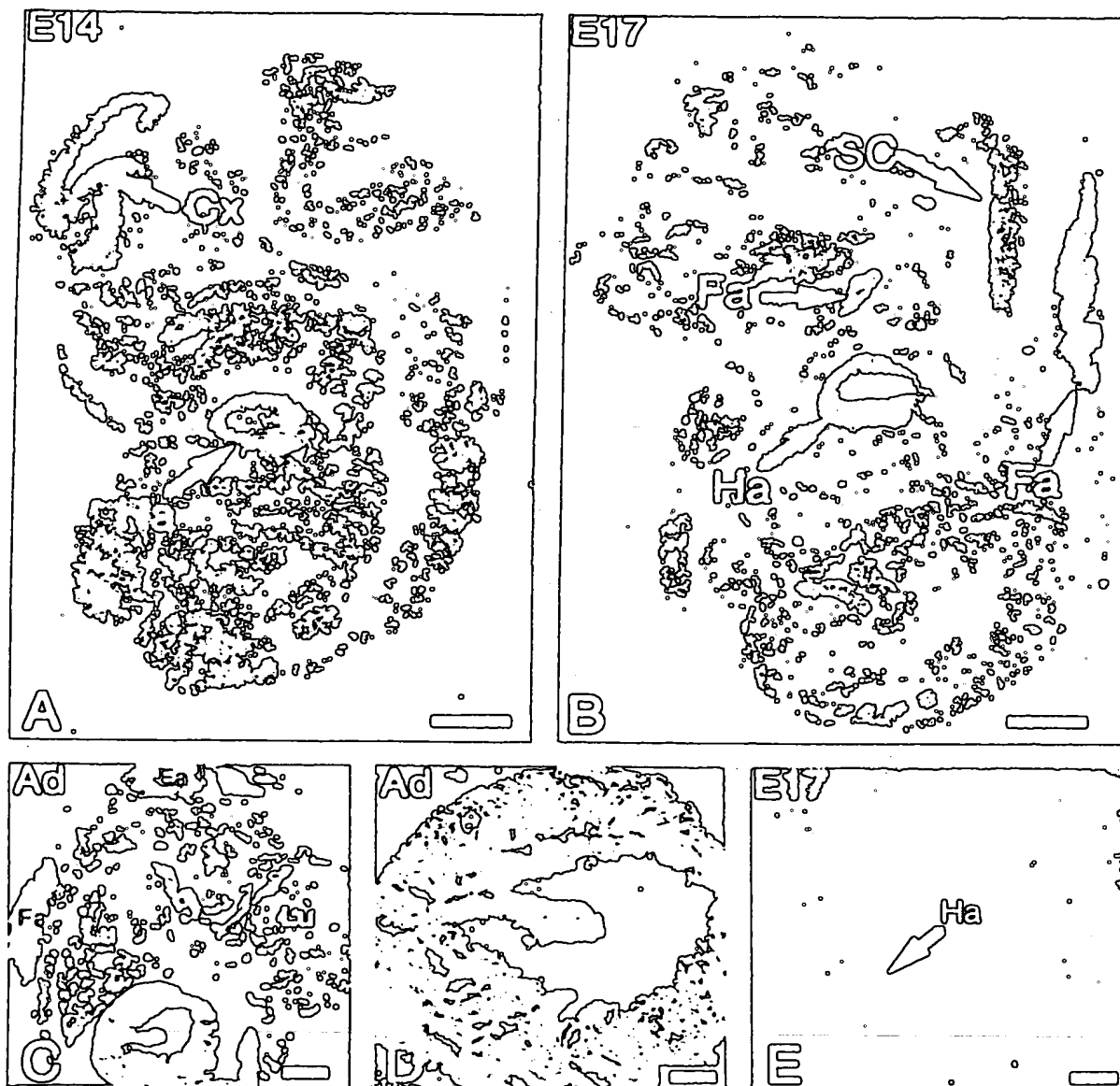
Fig.14
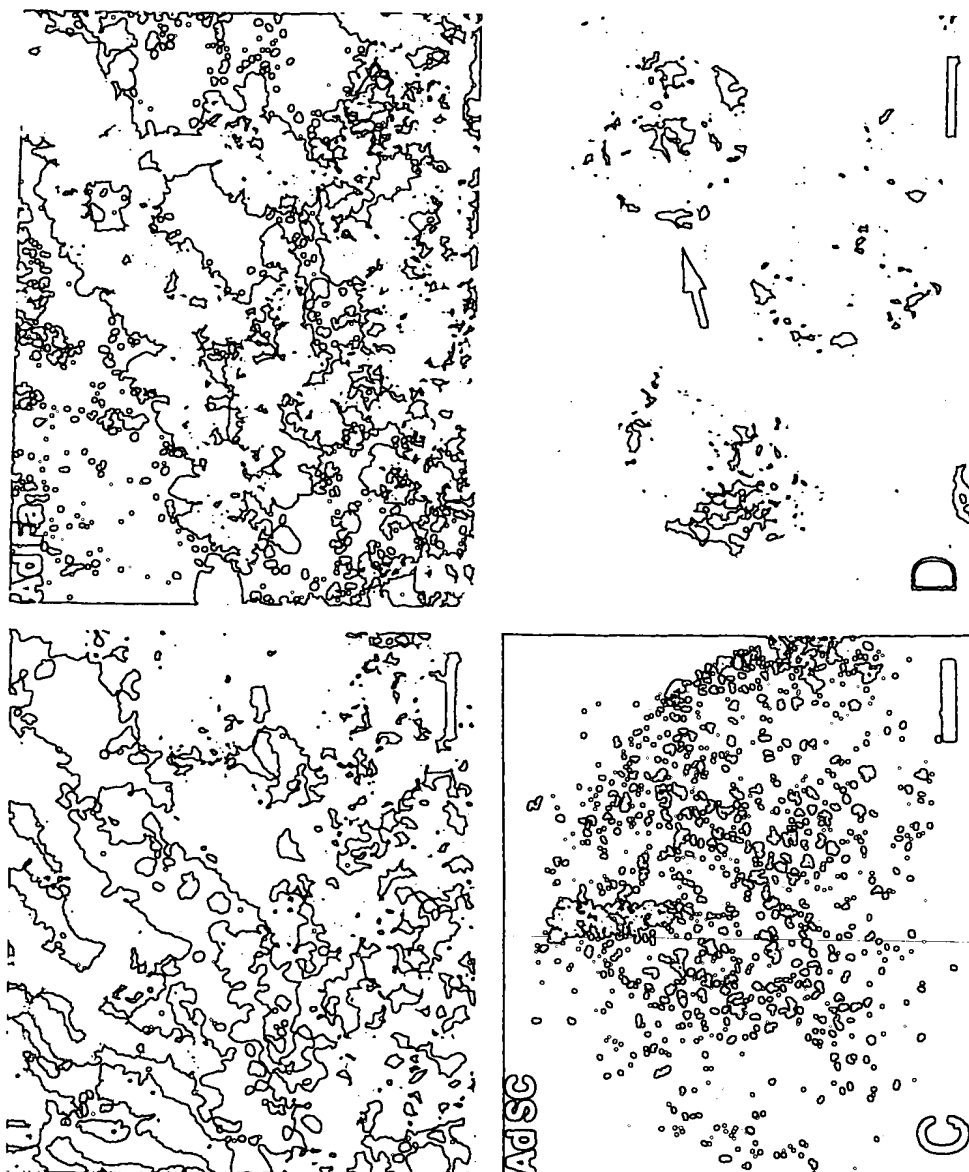
Fig. 15
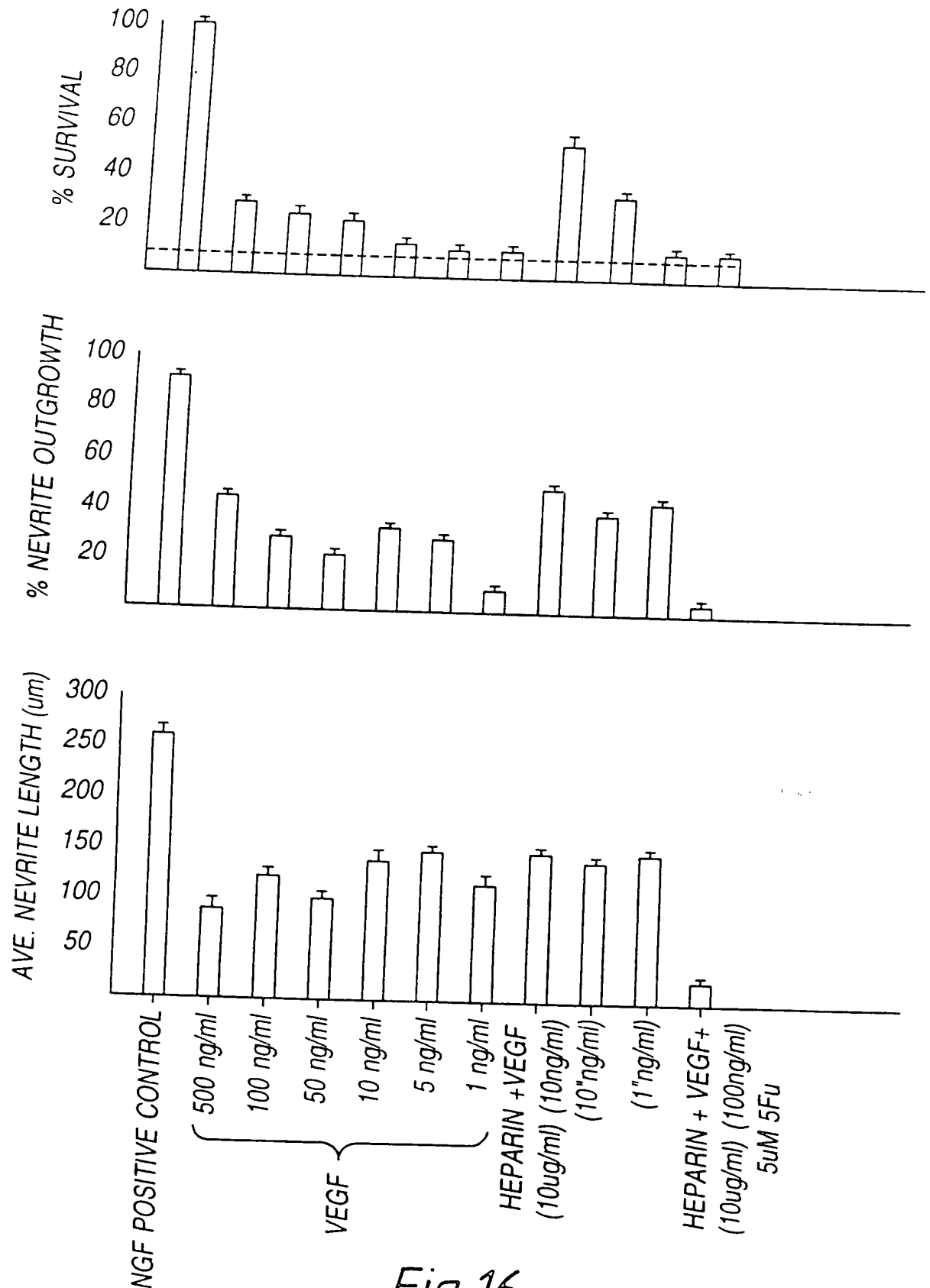
Fig.16
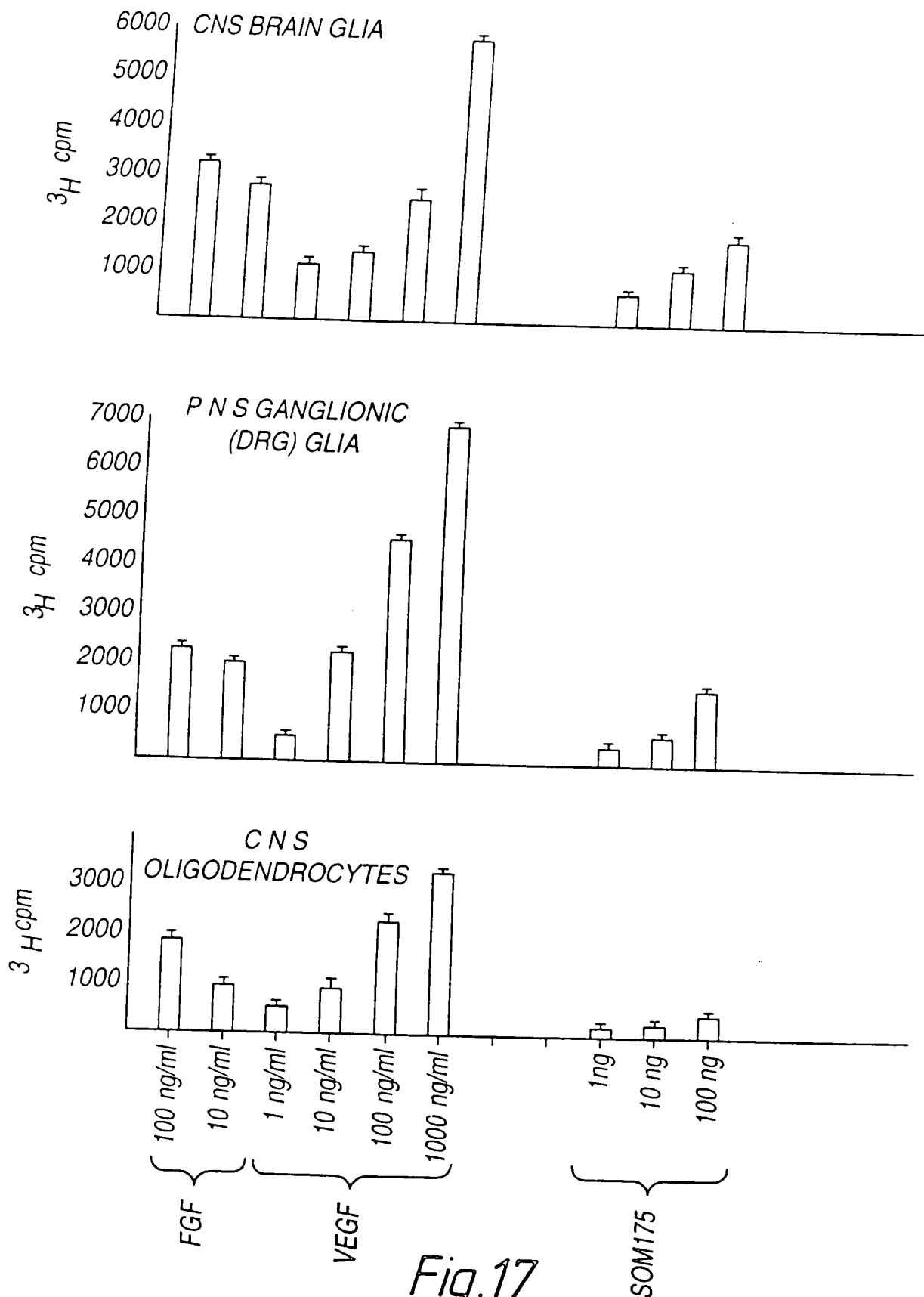
Fig.17
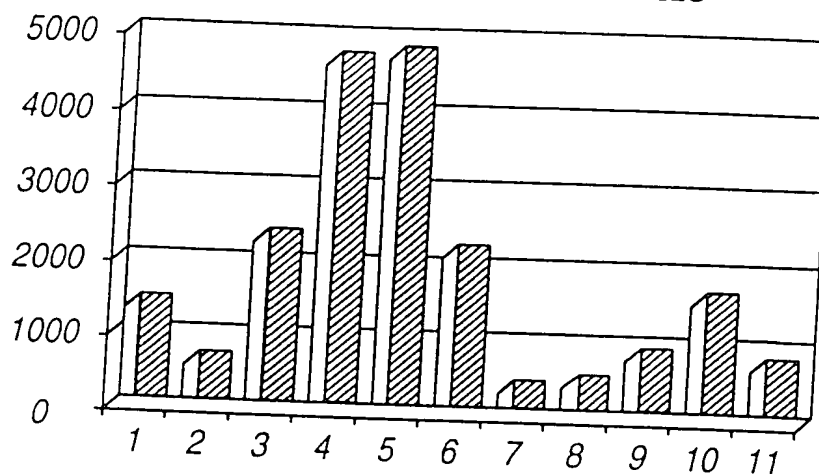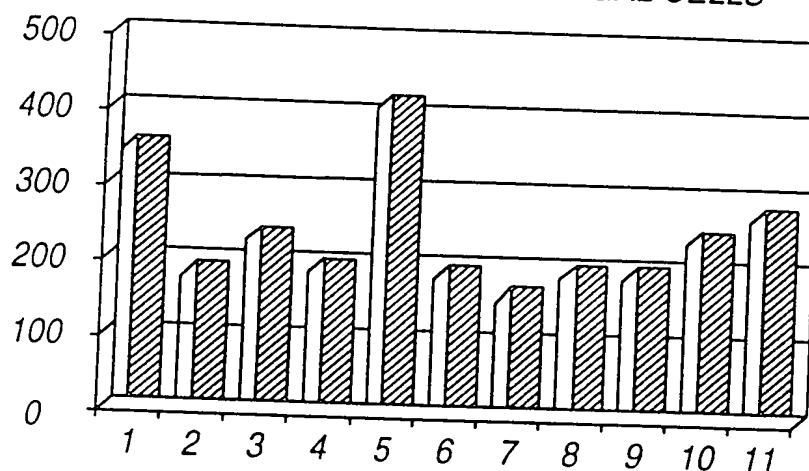
MOUSE ASTROGLIAL CELLS

Fig.18

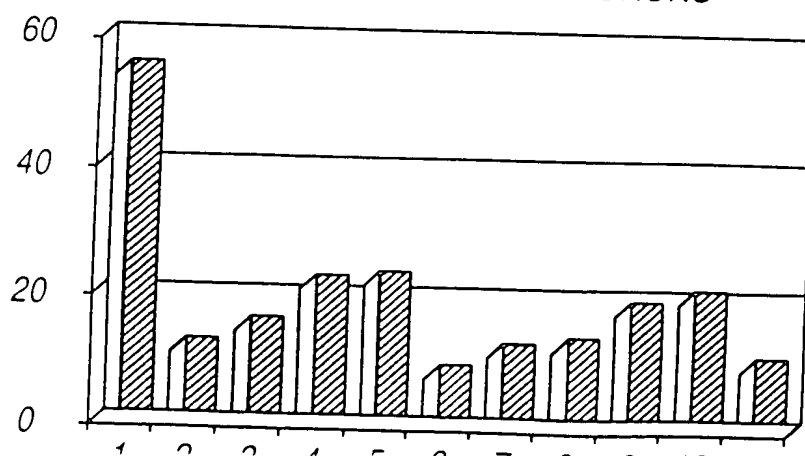## MOUSE OLIGODENDROGLIAL CELLS

Fig.19

MOUSE FOREBRAIN NEURONS

Fig.20